RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _/0/079,241A_
Source: _1Fw16_
Date Processed by STIC: _4/26/06_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 04/26/2006
PATENT APPLICATION: US/10/079,241A   TIME: 11:14:57

Input Set : A:\Revised sequence listing2.txt
Output Set: N:\CRF4\04262006\J079241A.raw

```
 3 <110> APPLICANT: Stratagene
 5 <120> TITLE OF INVENTION: HIGH FIDELITY DNA POLYMERASE COMPOSITIONS AND USES THEREFOR
 7 <130> FILE REFERENCE: 25436/2155
 9 <140> CURRENT APPLICATION NUMBER: 10/079,241A
10 <141> CURRENT FILING DATE: 2002-02-20
12 <160> NUMBER OF SEQ ID NOS: 23
14 <170> SOFTWARE: PatentIn version 3.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 7
18 <212> TYPE: PRT
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Conserved domain
24 <220> FEATURE:
25 <221> NAME/KEY: MISC_FEATURE
26 <222> LOCATION: (2)..(3)
27 <223> OTHER INFORMATION: Conserved domain, X at potision 2 or 3 is any amino acid.
30 <400> SEQUENCE: 1
```

W--> 32 **Asp Xaa Xaa Ser Leu Tyr Pro**
```
33 1                   5
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 9
38 <212> TYPE: PRT
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Conserved domain
44 <220> FEATURE:
45 <221> NAME/KEY: MISC_FEATURE
46 <222> LOCATION: (2)..(7)
47 <223> OTHER INFORMATION: Conserved domain, X at position 2, 3, 4, or 7 is any amino
acid.
50 <400> SEQUENCE: 2
```

W--> 52 **Lys Xaa Xaa Xaa Asn Ser Xaa Tyr Gly**
```
53 1                   5
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 5
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: Conserved domain
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: (2)..(3)
67 <223> OTHER INFORMATION: Conserved domain, X at position 2 or 3 is any amino acid.
```

RAW SEQUENCE LISTING   DATE: 04/26/2006
PATENT APPLICATION: US/10/079,241A   TIME: 11:14:57

Input Set : **A:\Revised sequence listing2.txt**
Output Set: **N:\CRF4\04262006\J079241A.raw**

```
      70 <400> SEQUENCE: 3
W--> 72 Thr Xaa Xaa Gly Arg
      73 1               5
      76 <210> SEQ ID NO: 4
      77 <211> LENGTH: 6
      78 <212> TYPE: PRT
      79 <213> ORGANISM: Artificial Sequence
      81 <220> FEATURE:
      82 <223> OTHER INFORMATION: Conserved domain
      84 <220> FEATURE:
      85 <221> NAME/KEY: MISC_FEATURE
      86 <222> LOCATION: (2)..(2)
      87 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
      90 <400> SEQUENCE: 4
W--> 92 Tyr Xaa Asp Thr Asp Ser
      93 1               5
      96 <210> SEQ ID NO: 5
      97 <211> LENGTH: 3
      98 <212> TYPE: PRT
      99 <213> ORGANISM: Artificial Sequence
     101 <220> FEATURE:
     102 <223> OTHER INFORMATION: Conserved domain
     104 <220> FEATURE:
     105 <221> NAME/KEY: misc_feature
     106 <222> LOCATION: (2)..(2)
     107 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
     110 <400> SEQUENCE: 5
W--> 112 Lys Xaa Tyr
     113 1
     116 <210> SEQ ID NO: 6
     117 <211> LENGTH: 4
     118 <212> TYPE: PRT
     119 <213> ORGANISM: Artificial Sequence
     121 <220> FEATURE:
     122 <223> OTHER INFORMATION: Conserved domain
     124 <220> FEATURE:
     125 <221> NAME/KEY: MISC_FEATURE
     126 <222> LOCATION: (2)..(2)
     127 <223> OTHER INFORMATION: Conserved domain, X at position 2 is any amino acid.
     130 <400> SEQUENCE: 6
W--> 132 Tyr Xaa Gly Gly
     133 1
     136 <210> SEQ ID NO: 7
     137 <211> LENGTH: 6
     138 <212> TYPE: PRT
     139 <213> ORGANISM: Artificial Sequence
     141 <220> FEATURE:
     142 <223> OTHER INFORMATION: Conserved domain
     144 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 04/26/2006
PATENT APPLICATION: US/10/079,241A   TIME: 11:14:57

Input Set : A:\Revised sequence listing2.txt
Output Set: N:\CRF4\04262006\J079241A.raw

```
145 <221> NAME/KEY: MISC_FEATURE
146 <222> LOCATION: (1)..(6)
147 <223> OTHER INFORMATION: Conserved domain
150 <400> SEQUENCE: 7
152 Ser Tyr Thr Gly Gly Phe
153 1               5
156 <210> SEQ ID NO: 8
157 <211> LENGTH: 23
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Synthetic primer
164 <220> FEATURE:
165 <221> NAME/KEY: misc_feature
166 <222> LOCATION: (1)..(23)
167 <223> OTHER INFORMATION: Synthetic primer
170 <400> SEQUENCE: 8
171 gaggagagca ggaaaggtgg aag                              23
174 <210> SEQ ID NO: 9
175 <211> LENGTH: 23
176 <212> TYPE: DNA
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Synthetic primer
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <222> LOCATION: (1)..(23)
185 <223> OTHER INFORMATION: Synthetic primer
188 <400> SEQUENCE: 9
189 gaggtacagg gttgaggcta ctg                              23
192 <210> SEQ ID NO: 10
193 <211> LENGTH: 776
194 <212> TYPE: PRT
195 <213> ORGANISM: Thermococcus sp. JDF-3
197 <400> SEQUENCE: 10
199 Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Asn Gly Lys Pro Val Ile
200 1               5                   10                  15
203 Arg Val Phe Lys Lys Glu Asn Gly Glu Phe Arg Ile Glu Tyr Asp Arg
204             20                  25                  30
207 Glu Phe Glu Pro Tyr Phe Tyr Ala Leu Leu Arg Asp Asp Ser Ala Ile
208             35                  40                  45
211 Glu Glu Ile Lys Lys Ile Thr Ala Glu Arg His Gly Arg Val Val Lys
212     50                  55                  60
215 Val Lys Arg Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Ser Val
216 65                  70                  75                  80
219 Glu Val Trp Val Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
220             85                  90                  95
223 Arg Asp Lys Ile Arg Lys His Pro Ala Val Ile Asp Ile Tyr Glu Tyr
224             100                 105                 110
```

```
227 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
228         115             120             125
231 Met Glu Gly Glu Glu Glu Leu Lys Leu Met Ser Phe Asp Ile Glu Thr
232     130             135             140
235 Leu Tyr His Glu Gly Glu Glu Phe Gly Thr Gly Pro Ile Leu Met Ile
236 145             150             155             160
239 Ser Tyr Ala Asp Glu Ser Glu Ala Arg Val Ile Thr Trp Lys Lys Ile
240             165             170             175
243 Asp Leu Pro Tyr Val Glu Val Val Ser Thr Glu Lys Glu Met Ile Lys
244         180             185             190
247 Arg Phe Leu Arg Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
248         195             200             205
251 Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu
252     210             215             220
255 Lys Leu Gly Val Ser Phe Thr Leu Gly Arg Asp Gly Ser Glu Pro Lys
256 225             230             235             240
259 Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Val
260             245             250             255
263 His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
264         260             265             270
267 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Val Phe Gly Lys Pro Lys Glu
268         275             280             285
271 Lys Val Tyr Ala Glu Glu Ile Ala Thr Ala Trp Glu Thr Gly Glu Gly
272     290             295             300
275 Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Arg Val Thr Tyr
276 305             310             315             320
279 Glu Leu Gly Arg Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
280             325             330             335
283 Ile Gly Gln Gly Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
284         340             345             350
287 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
288         355             360             365
291 Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Gly Gly Tyr
292     370             375             380
295 Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Asp Asn Ile
296 385             390             395             400
299 Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
300             405             410             415
303 Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Ser Tyr Asp
304         420             425             430
307 Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
308         435             440             445
311 Ile Pro Ser Leu Leu Gly Asn Leu Leu Glu Glu Arg Gln Lys Ile Lys
312     450             455             460
315 Arg Lys Met Lys Ala Thr Leu Asp Pro Leu Glu Lys Asn Leu Leu Asp
316 465             470             475             480
319 Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly Tyr
320             485             490             495
323 Tyr Gly Tyr Ala Arg Ala Arg Trp Tyr Cys Arg Glu Cys Ala Glu Ser
```

```
324              500              505              510
327 Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Met Val Ile Arg Glu Leu
328          515              520              525
331 Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Leu
332      530              535              540
335 His Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
336 545              550              555              560
339 Met Glu Phe Leu Asn Tyr Ile Asn Pro Lys Leu Pro Gly Leu Leu Glu
340              565              570              575
343 Leu Glu Tyr Glu Gly Phe Tyr Val Arg Gly Phe Phe Val Thr Lys Lys
344          580              585              590
347 Lys Tyr Ala Val Ile Asp Glu Glu Gly Lys Ile Thr Thr Arg Gly Leu
348          595              600              605
351 Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
352      610              615              620
355 Arg Val Leu Glu Ala Ile Leu Arg His Gly Asp Val Glu Glu Ala Val
356 625              630              635              640
359 Arg Ile Val Arg Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
360              645              650              655
363 Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Glu Leu Lys Asp
364          660              665              670
367 Tyr Lys Ala Thr Gly Pro His Val Ala Ile Ala Lys Arg Leu Ala Ala
368          675              680              685
371 Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
372      690              695              700
375 Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
376 705              710              715              720
379 Asp Pro Thr Lys His Lys Tyr Asp Ala Asp Tyr Tyr Ile Glu Asn Gln
380              725              730              735
383 Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
384          740              745              750
387 Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
388          755              760              765
391 Leu Lys Pro Lys Gly Lys Lys Lys
392      770              775
395 <210> SEQ ID NO: 11
396 <211> LENGTH: 2331
397 <212> TYPE: DNA
398 <213> ORGANISM: Thermococcus sp. JDF-3
400 <400> SEQUENCE: 11
401 atgatccttg acgttgatta catcaccgag aatggaaagc ccgtcatcag ggtcttcaag      60
403 aaggagaacg gcgagttcag gattgaatac gaccgcgagt tcgagcccta cttctacgcg     120
405 ctcctcaggg acgactctgc catcgaagaa atcaaaaaga taaccgcgga gaggcacggc     180
407 agggtcgtta aggttaagcg cgcggagaag gtgaagaaaa agttcctcgg caggtctgtg     240
409 gaggtctggg tcctctactt cacgcacccg caggacgttc cggcaatccg cgacaaaata     300
411 aggaagcacc ccgcggtcat cgacatctac gagtacgaca taccttcgc caagcgctac     360
413 ctcatagaca agggcctaat cccgatggaa ggtgaggaag agcttaaact catgtccttc     420
415 gacatcgaga cgctctacca cgagggagaa gagtttggaa ccgggccgat tctgatgata     480
417 agctacgccg atgaaagcga ggcgcgcgtg ataacctgga agaagatcga ccttccttac     540
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/26/2006
PATENT APPLICATION: US/10/079,241A   TIME: 11:14:59

Input Set : **A:\Revised sequence listing2.txt**
Output Set: **N:\CRF4\04262006\J079241A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3
Seq#:2; Xaa Pos. 2,3,4,7
Seq#:3; Xaa Pos. 2,3
Seq#:4; Xaa Pos. 2
Seq#:5; Xaa Pos. 2
Seq#:6; Xaa Pos. 2
Seq#:17; Xaa Pos. 2,3
Seq#:20; Xaa Pos. 2

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,20

VERIFICATION SUMMARY   DATE: 04/26/2006
PATENT APPLICATION: **US/10/079,241A**   TIME: 11:14:59

Input Set : **A:\Revised sequence listing2.txt**
Output Set: **N:\CRF4\04262006\J079241A.raw**

```
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:593 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
```